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Seliwiorstow, Tomasz; Uyttendaele, Mieke; Nauta, Maarten; De Zutter, Lieven

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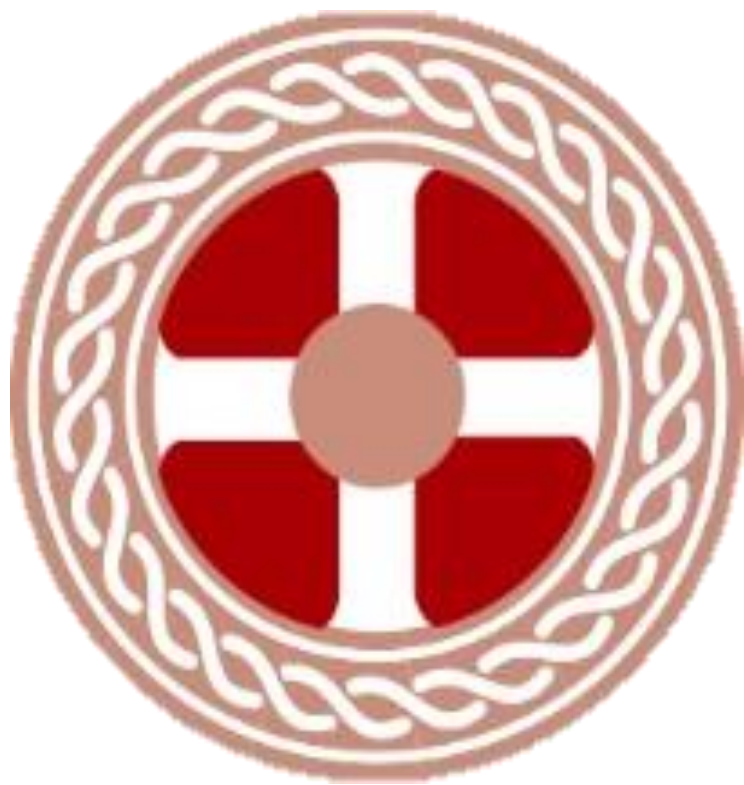
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Evaluation of risk-based microbiological criteria for *Campylobacter* in broiler carcasses in Belgium using TRiMiCri

Tomasz Seliwiorstow^{a,b}, Mieke Uyttendaele^b, Lieven De Zutter^a and Maarten Nauta^c

^aDepartment of Veterinary Public Health and Food Safety, Faculty of Veterinary Medicine, Ghent University, Merelbeke, Belgium
^bDepartment of Food Safety and Food Quality, Faculty of Bioscience Engineering, Ghent University, Belgium
^cRisk-Benefit Research Group, National Food Institute, Technical University of Denmark, Denmark

contact: maana@food.dtu.dk
tomasz.seliwiorstow@ugent.be



Introduction

Campylobacter is the most commonly reported gastrointestinal bacterial pathogen in humans in many industrialized countries. The majority of human infections is attributed to consumption and handling of the contaminated poultry meat. Additionally, the relationship between in particular elevated *Campylobacter* numbers on broiler meat and consumers’ health risk is established. As such, preventing consumers from highly contaminated products by setting a microbiological criterion for *Campylobacter* on broiler meat can be an effective tool to reduce the number of human campylobacteriosis^{1,2}. If this criterion is based on risk assessment and estimates the effect on public health risk, it is called risk-based microbiological criterion (MC). To establish risk-based MCs, the availability of a quantitative microbiological risk assessment (QMRA) model is required. However, QMRA technique is time consuming and often requires extensive modeling expertise. To facilitate the use of risk-based MCs for *Campylobacter*, a software tool (TRiMiCri) has recently been made available and can be downloaded freely (<http://tools.food.dtu.dk/trimicri>).

Objectives

In this present study TRiMiCri was used to evaluate risk-based microbiological criteria using *Campylobacter* data collected in Belgium.

Methods

Campylobacter quantitative data

- 6 Belgian slaughterhouses
- 28 *Campylobacter* positive batches
- 5 batches per slaughterhouse except for slaughterhouse C (3 batches)
- Breast skin from 6 carcasses after chilling per batch
- Enumeration limit = 10 cfu/g

Campylobacter baseline data (2008 EU baseline study)

- 9 Belgian slaughterhouses
- 389 carcasses after chilling were sampled; one carcass per batch
- Breast and neck skin
- Enumeration (limit = 10cfu/g) and detection (enrichment)

TRiMiCri Tool for Risk-based Microbiological Criteria

- Allows testing broiler meat batches for compliance against risk-based MCs for *Campylobacter*, even if the number of samples taken *N* is larger than the predefined *n*
- The evaluation is based on quantitative data from skin samples collected after slaughter
- TRiMiCri applies the QMRA model presented by Nauta *et al.* (2015)². It allows an evaluation of two types of MCs:

1. **Microbiological Limit MC (ML-MC)** - the batch is not complying if more than *c* out of *n* product samples contain more than *m* cfu/g.
2. **Relative Risk Limit MC (RRL-MC)** - The batch is not complying if the relative risk (RR) estimate for *n* product samples is larger than a critical relative risk RR_{crit} . RR_{crit} is calculated as the risk estimate of the batch divided by the baseline risk

¹Nauta, Sanaa, and Havelaar, 2012, Int. J. Food Microb 158:209-217; ² Nauta et al. 2015 Food Control 53:177-184.

Conclusions

- TriMiCri is a user friendly software tool that allows the evaluation of broiler meat batches against different risk-based MCs, based on own sample data.
- As an example, when taking *Campylobacter* prevalence into account, approximately one-third of all produced batches in Belgium are non-complying with the ML-MC (*n*=6, *m*=1000, *c*=0) and MC-RRL (*n*=6, RRL=1). In Belgium, non-complying batches were distributed almost equally between slaughterhouses.
- A risk-based MC should be based on the balance between potential risk reduction (benefit) and the percentage of non-complying batches (cost). TRiMiCri facilitates risk managers in the selection of this MC.

Results

Table 1.

Results for six ML-MC scenarios. Red color indicates no compliance of the batch with chosen criterion. If $N=n$ (like in this case), no Monte Carlo simulation is done, either 100% or 0% is complying.

Sl.	Batch	<i>n</i> =6, <i>c</i> =0, <i>m</i> =100	<i>n</i> =6, <i>c</i> =0, <i>m</i> =1000	<i>n</i> =6, <i>c</i> =0, <i>m</i> =10000	<i>n</i> =6, <i>c</i> =1, <i>m</i> =100	<i>n</i> =6, <i>c</i> =1, <i>m</i> =1000	<i>n</i> =6, <i>c</i> =1, <i>m</i> =10000
A	A1	0	0	0	0	0	0
	A2	0	100	100	0	100	100
	A3	0	0	100	0	0	100
	A4	0	0	100	0	0	100
	A5	100	100	100	100	100	100
B	B1	0	0	0	0	0	0
	B2	0	100	100	0	100	100
	B3	0	0	100	0	0	100
	B4	0	0	100	0	0	100
	B5	0	100	100	0	100	100
C	C1	0	0	0	0	0	100
	C2	0	0	0	0	0	0
	C3	0	0	100	0	0	100
D	D1	0	0	0	0	0	100
	D2	0	100	100	0	100	100
	D3	0	100	100	0	100	100
	D4	0	0	100	0	100	100
	D5	0	0	100	0	100	100
E	E1	0	100	100	0	100	100
	E2	0	0	0	0	0	0
	E3	0	0	100	0	100	100
	E4	0	0	100	0	100	100
	E5	0	100	100	100	100	100
F	F1	0	0	100	0	0	100
	F2	0	0	0	0	0	100
	F3	0	100	100	0	100	100
	F4	0	0	0	0	0	100
	F5	0	100	100	0	100	100

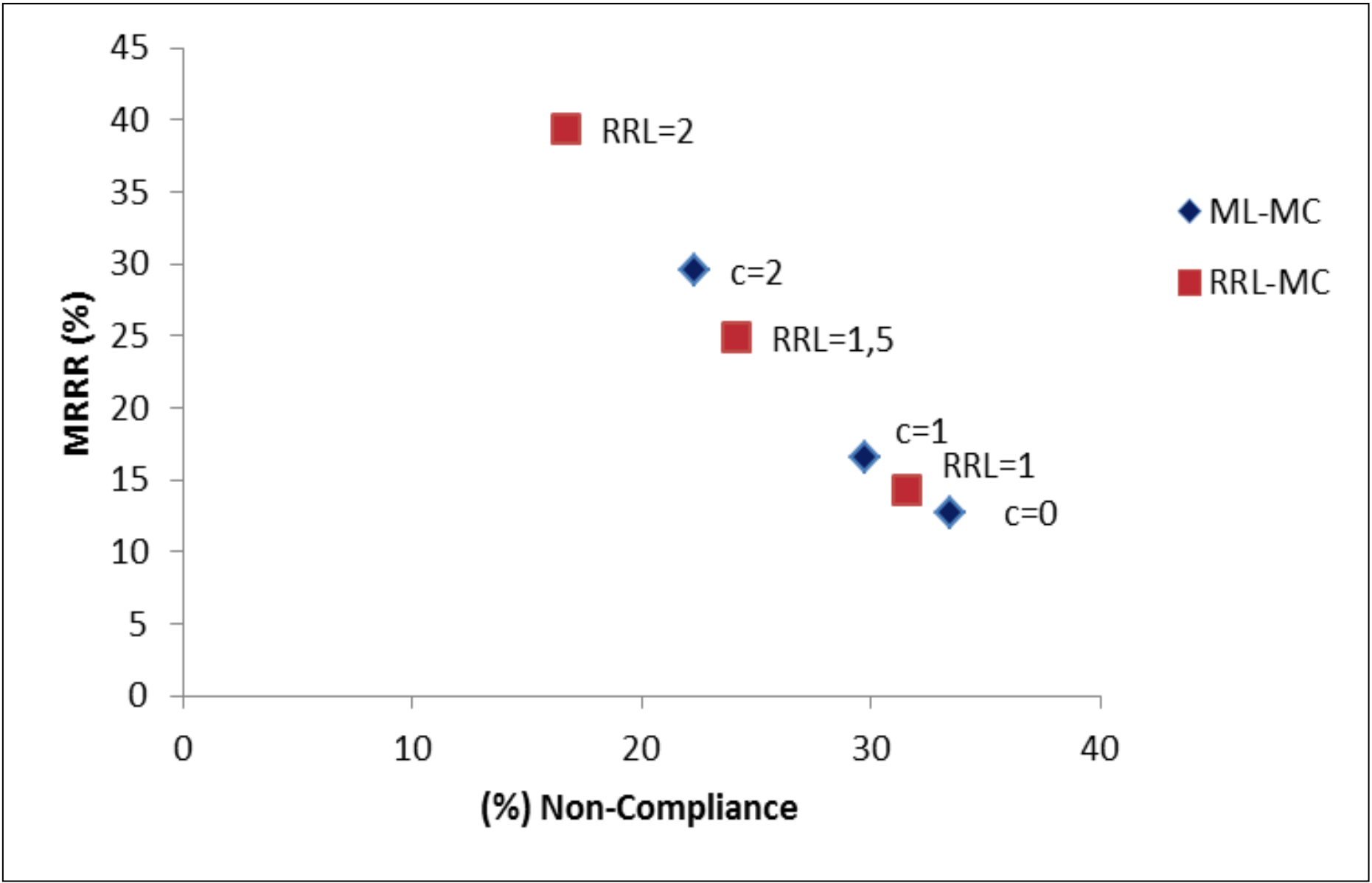
Table 2.

Results for six RRL-MC scenarios. Red color indicates no compliance of the batch with chosen criterion. If $N>n$, results 100 (or 0) imply that batches do comply in all (or none of) the Monte-Carlo simulations performed.

Sl.	Batch	Relative Risk	<i>n</i> =6, RRL=1	<i>n</i> =6, RRL=1.5	<i>n</i> =6, RRL=2	<i>n</i> =5, RRL=1	<i>n</i> =5, RRL=1.5	<i>n</i> =5, RRL=2
A	A1	5.356	0	0	0	0	0	0
	A2	0.799	100	100	100	100	100	100
	A3	1.466	0	100	100	0	51	100
	A4	1.821	0	0	100	0	0	83
	A5	0.213	100	100	100	100	100	100
B	B1	3.731	0	0	0	0	0	0
	B2	1.078	0	100	100	0	100	100
	B3	1.944	0	0	100	0	0	67
	B4	1.576	0	0	100	0	17	100
	B5	0.441	100	100	100	100	100	100
C	C1	2.696	0	0	0	0	0	0
	C2	3.860	0	0	0	0	0	0
	C3	1.503	0	0	100	0	67	100
D	D1	2.073	0	0	0	0	16	16
	D2	0.741	100	100	100	100	100	100
	D3	0.830	100	100	100	100	100	100
	D4	2.361	0	0	0	0	0	0
	D5	0.817	100	100	100	100	100	100
E	E1	0.420	100	100	100	100	100	100
	E2	3.220	0	0	0	0	0	16
	E3	0.963	100	100	100	67	100	100
	E4	1.299	0	100	100	0	82	100
	E5	0.287	100	100	100	100	100	100
F	F1	1.197	0	100	100	16	0	100
	F2	3.057	0	0	0	0	0	0
	F3	0.500	100	100	100	100	100	100
	F4	2.374	0	0	0	0	0	16
	F5	0.738	100	100	100	100	100	100

Figure 1.

The relationship between the percentage of non-complying batches and minimum relative residual risk (MRRR) for 3 ML-MC (*n*=6, *m*=1000, *c*=0, 1, 2) and 3 RRL-MC scenarios (*n*=6, RRL=1, 1.5, 2). The *Campylobacter* prevalence is taken into account when estimating the percentage of non-complying batches



MRRR – the quotient of the mean risk of all batches complying with the MC and the mean risk of the whole set of batches. It is a minimum risk because it refers to the situation where all batches are sampled and all noncomplying batches undergo treatment that effectively eliminates *Campylobacter* and are replaced by zero risk batches - if some non-complying batches would slip through, the relative residual risk would be higher.